1. (Currently Amended) A method for mapping a gene network comprising the steps of:

preparing a plurality of biological samples;

detecting ~~and comparing the~~ expression of at least ~~5~~ five genes in said biological

samples;

comparing expression of the at least five genes in a first of said biological samples

to expression of the at least five genes in a second of said biological samples;

generating a cluster map for said genes, wherein the cluster map categorizes genes

according to ~~the~~ similarity ~~correlation~~ in unchanged, increased, or decreased expression

~~among said genes~~ in the first relative to the second of said biological samples; and

analyzing said cluster map to generate gene network causal models defining

regulatory relationships among said genes.

2. (Currently Amended) The method of claim 1, wherein ~~expression of said genes is~~

~~detected by measuring the relative and/ or~~ absolute amount of transcripts of said genes in

each of the biological samples is determined and compared.

3. (Original) The method of claim 2, wherein said amount of transcripts is detected with a

high density nucleic acid array.

4. (Original) The method of claim 1, wherein said biological samples are prepared by a

homozygous knockout strategy.

5. (Currently Amended) The method of claim 1, wherein each of said biological samples

is derived from one clone of ~~said~~ cells.

6. (Original) The method of claim 1, wherein said biological samples are prepared using cells representing different developmental, physiological or pathological status.

7. (Original) The method of claim 1, wherein said biological samples are prepared by stimulating cells with a combination of a plurality of hormones.

8. (Original) The method of claim 1, wherein said biological samples are prepared by transfecting cells with a combination of a plurality of vectors, said vectors being used by said cells as templates to transcribe a plurality of RNAs, each of said RNAs having a sequence complementary to one of said genes.

9. (Original) The method of claim 1, wherein said gene network causal models are generated and tested using the Linear Structure Relations (LISREL) process performed in a digital computer.

10-105. Withdrawn.

106. (Original) The method of claim 7̶ 1 wherein said biological samples are prepared using random chemical mutagenesis.

107. (Original) The method of claim 7̶ 1 wherein said biological samples are prepared using microinjection of antisense RNA or protein into cells.